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Page of
#10

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT-IN-REEXAMINATION	ATTORNEY DOCKET NO.
09/515,369 ✓	02/29/00	FISHER	0575/567787/J
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		HZ 12/0529 JUN - 1 2001	EXAMINER
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		PROV. REC'D. 1633	ART UNIT
			PAPER
			TECH CENTER
			JUN 12 2001

John P White
Cooper & Dunham LLP
1185 Avenue of the Americas
New York NY 10036

1m. 6.29.01
2m. 7.29.01
3m. 8.29.01
4m. 9.29.01
5m. 10.29.01
6m. 11.29.01

AP

9
05/29/01

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

The communication filed on [April 2, 2001] is not fully responsive to the Office communication mailed [February 23, 2001] for the reason(s) set forth on the attached Notice to Comply With the Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of ONE (1) MONTH from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner Eleanor Sorbello, Art Unit 1633, whose telephone number is (703) 308-6043. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Deborah Clark whose telephone number is (703) 305-4051. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

Deborah Clark
DEBORAH J. R. CLARK
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

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TECH CENTER 1600
JUN 21 2001

Notice to Comply

Application No.

09/575,369

Applicant(s)

Examiner

Art Unit

1633

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES

Applicant must file the items indicated below within the time period set by the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other:

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Orbelle

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

#61309
513101



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/515,369

RECEIVED

Source: 1633

MAY - 1 2001

Date Processed by STIC: 4/22/2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

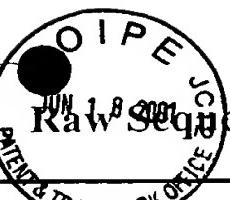
TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>



Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/515,369

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--------------------------------------|--|
| 1 | ____ Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | ____ Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | ____ Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | ____ Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | ____ Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | ____ Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 | ____ PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 8 | ____ Skipped Sequences (OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | ____ Skipped Sequences (NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 10 | ____ Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 | ____ Use of "Artificial" (NEW RULES) | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence. |
| 12 | ____ Use of <220>Feature (NEW RULES) | Sequence(s) <u>2-13</u> are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | ____ PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\1515369.raw

Does Not Comply
Corrected Diskette Needed



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

91 ~~tttactccat~~ cccaggcttc atctcacctc aggggctgct ttccccatcg ctgtattgtc 2100
93 cttaaaggta tgggtgacta ggcaatgaag taattctcta gaaaggcatg accaatttcc 2160
95 ctttctccac ctccctcttt ttccctccacc cctccccat cagccccat atatatgcc 2220
97 aaatctccac aaagccttgc ttgcctgcaa acctttactt ctgaaatgac ttccacggct 2280
99 gggacg 2286

102 <210> SEQ ID NO: 2

103 <211> LENGTH: 21

104 <212> TYPE: DNA

> 105 <213> ORGANISM: Artificial

> 107 <220> FEATURE:

> 107 <223> OTHER INFORMATION:

107 <400> SEQUENCE: 2

108 cgtccccagcc gtggaaagtca t

111 <210> SEQ ID NO: 3

112 <211> LENGTH: 21

113 <212> TYPE: DNA

> 114 <213> ORGANISM: Artificial

> 116 <220> FEATURE:

> 116 <223> OTHER INFORMATION:

116 <400> SEQUENCE: 3

117 aggctggatt tggcttgtga c

120 <210> SEQ ID NO: 4

121 <211> LENGTH: 21

122 <212> TYPE: DNA

> 123 <213> ORGANISM: Artificial

> 125 <220> FEATURE:

> 125 <223> OTHER INFORMATION:

125 <400> SEQUENCE: 4

126 ctgttaatc cagcaacttcc c

129 <210> SEQ ID NO: 5

130 <211> LENGTH: 21

131 <212> TYPE: DNA

> 132 <213> ORGANISM: Artificial

> 134 <220> FEATURE:

> 134 <223> OTHER INFORMATION:

134 <400> SEQUENCE: 5

135 cgcttgatga ctcagccgga a

138 <210> SEQ ID NO: 6

139 <211> LENGTH: 20

140 <212> TYPE: DNA

> 141 <213> ORGANISM: Artificial

> 143 <220> FEATURE:

> 143 <223> OTHER INFORMATION:

143 <400> SEQUENCE: 6

144 tgcagatgc gcaatctgca

147 <210> SEQ ID NO: 7

148 <211> LENGTH: 21

149 <212> TYPE: DNA

> 150 <213> ORGANISM: Artificial

(global errors)

see item 11 on Ema Summary Sheet

→ see item 12 on Ema Summary Sheet

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

```

> 152 <220> FEATURE:
> 152 <223> OTHER INFORMATION:
152 <400> SEQUENCE: 7
153 cgcttggatga ctggccgga a 21
156 <210> SEQ ID NO: 8
157 <211> LENGTH: 22
158 <212> TYPE: DNA
> 159 <213> ORGANISM: Artificial
> 161 <220> FEATURE:
> 161 <223> OTHER INFORMATION:
161 <400> SEQUENCE: 8
162 tgcagagaga cttagtctctg ca 22
165 <210> SEQ ID NO: 9
166 <211> LENGTH: 61
167 <212> TYPE: DNA
> 168 <213> ORGANISM: Artificial
> 170 <220> FEATURE:
> 170 <223> OTHER INFORMATION:
170 <400> SEQUENCE: 9
171 uuguauuuau uacaacucua uuuaauuaau gucaguauuu caacugaagu ucuaauuaau 60
173 u 61
176 <210> SEQ ID NO: 10
177 <211> LENGTH: 15
178 <212> TYPE: DNA
> 179 <213> ORGANISM: Artificial
> 181 <220> FEATURE:
> 181 <223> OTHER INFORMATION:
181 <400> SEQUENCE: 10
182 uauuuauuuu uuuaa 15
185 <210> SEQ ID NO: 11
186 <211> LENGTH: 51
187 <212> TYPE: DNA
> 188 <213> ORGANISM: Artificial
> 190 <220> FEATURE:
> 190 <223> OTHER INFORMATION:
190 <400> SEQUENCE: 11
191 uaaaaauuuau auauuuauuu uuuuaaaaaua uuuauuuauu uaaaaauuuua a 51
194 <210> SEQ ID NO: 12
195 <211> LENGTH: 34
196 <212> TYPE: DNA
> 197 <213> ORGANISM: Artificial
> 199 <220> FEATURE:
> 199 <223> OTHER INFORMATION:
199 <400> SEQUENCE: 12
200 auuauuuauu auuauuuau uuuuuauuuua uuuu 34
203 <210> SEQ ID NO: 13
204 <211> LENGTH: 56
205 <212> TYPE: DNA
> 206 <213> ORGANISM: Artificial

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

> 208 <220> FEATURE:
> 208 <223> OTHER INFORMATION:
208 <400> SEQUENCE: 13
209 guuuuuuaauu uauuuauuaa gauggauucu cagauauuuua uauuuuuauu uuauuu

56



VERIFICATION SUMMARY
PATENT APPLICATION: US 369,369

DATE: 04/22/2001
TIME: 14:17:04

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

L05 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L07 M:258 W: Mandatory Feature missing, <220> FEATURE:
L07 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L14 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L16 M:258 W: Mandatory Feature missing, <220> FEATURE:
L16 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L23 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L25 M:258 W: Mandatory Feature missing, <220> FEATURE:
L25 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L32 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L34 M:258 W: Mandatory Feature missing, <220> FEATURE:
L34 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L41 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L43 M:258 W: Mandatory Feature missing, <220> FEATURE:
L43 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L50 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L52 M:258 W: Mandatory Feature missing, <220> FEATURE:
L52 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L59 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L61 M:258 W: Mandatory Feature missing, <220> FEATURE:
L61 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L68 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L70 M:258 W: Mandatory Feature missing, <220> FEATURE:
L70 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L79 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
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L90 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L97 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L99 M:258 W: Mandatory Feature missing, <220> FEATURE:
L99 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
206 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
208 M:258 W: Mandatory Feature missing, <220> FEATURE:
208 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: